

## 09786635 Results

SEQ ID NO: 1

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6880	100.0	6880	6	AX253450	AX253450 Sequence
2	6880	100.0	6880	9	HSA012376	AJ012376 Homo sapi
3	6880	100.0	7260	6	AX253452	AX253452 Sequence
4	6879	100.0	9497	6	AX059973	AX059973 Sequence
5	6879	100.0	9497	9	AF165281	AF165281 Homo sapi
6	6875.8	99.9	9741	6	AX127830	AX127830 Sequence
7	6875.8	99.9	9741	6	AX139817	AX139817 Sequence
8	6875.8	99.9	9741	6	AX351038	AX351038 Sequence
9	6875.8	99.9	9854	6	AX127831	AX127831 Sequence
10	6875.8	99.9	9854	6	AX139818	AX139818 Sequence
11	6870.4	99.9	7860	6	AX092594	AX092594 Sequence
12	6865	99.8	9495	6	AX059978	AX059978 Sequence
13	6862.4	99.7	10442	6	AX060713	AX060713 Sequence
14	6862.4	99.7	10442	6	AX060892	AX060892 Sequence
15	6862.4	99.7	10442	9	AF285167	AF285167 Homo sapi
16	6860.8	99.7	10474	6	AX060719	AX060719 Sequence
17	6860.8	99.7	10474	6	AX060721	AX060721 Sequence
18	6860.8	99.7	10474	6	AX060898	AX060898 Sequence
19	6860.8	99.7	10474	6	AX060900	AX060900 Sequence
20	6845.2	99.5	7862	6	AX135712	AX135712 Sequence
21	6760.2	98.3	9593	6	AX059976	AX059976 Sequence
22	6711.6	97.6	6786	9	AB055982	AB055982 Homo sapi
23	5630	81.8	7878	10	MMABC1	X75926 Mus musculu
24	5455.6	79.3	6801	10	AY208182	AY208182 Rattus no
25	4302	62.5	7074	5	AF362377	AF362377 Gallus ga
26	2052.4	29.8	5097	6	BD012346	BD012346 Genes rel
27	2052.4	29.8	5097	6	BD160225	BD160225 Primer fo
28	2052.4	29.8	5097	9	AK027864	AK027864 Homo sapi
29	1911.6	27.8	7298	9	AF001945	AF001945 Homo sapi

## AF165281

LOCUS AF165281 9497 bp mRNA linear PRI 17-AUG-1999  
 DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA,  
 complete cds.

ACCESSION AF165281

VERSION AF165281.1 GI:5734100

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 9497)

AUTHORS Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,  
 Deleuze,J.F., Brewer,H.B., Duverger,N., Deneffe,P. and Assmann,G.

TITLE Tangier disease is caused by mutations in the gene encoding  
 ATP-binding cassette transporter 1

JOURNAL Nat. Genet. 22 (4), 352-355 (1999)

MEDLINE 99364413

PUBMED 10431238

REFERENCE 2 (bases 1 to 9497)

AUTHORS Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,  
 Deleuze,J.F., Brewer,H.B., Duverger,N., Deneffe,P. and Assmann,G.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston  
 Cr#mieux, Evry 91006, France

FEATURES Location/Qualifiers

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 /mol\_type="mRNA"

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CDS 121. .6726
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BASE COUNT      2600 a      2115 c      2217 g      2564 t          1 others
ORIGIN

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Query Match      100.0%; Score 6879; DB 9; Length 9497;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6879; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTAATGCCAACAAACCCC 180

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Db	301	AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	360
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Qy	661	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
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Db	721	TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTGAGCATGAGAAGCTGGAGTGAC	780
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Db	781	ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Qy	841	TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGCTGAAGATCAAG	900
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Db	901	TCTCTCAACTGGTATGAGGACAACAACCTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
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Qy	1021	AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Db	1021	AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Qy	1081	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Db	1081	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Qy	1141	AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
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Db	3061	CTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCTTCTGGATGAACCCACA	3120
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Qy	3181	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240
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 Db 4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260  
 Qy 4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCCTTCA 4320  
 |||||  
 Db 4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCCTTCA 4320  
 Qy 4321 CCTGCATGCCAGTGTAGCAGCGACAAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380  
 |||||  
 Db 4321 CCTGCATGCCAGTGTAGCAGCGACAAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380  
 Qy 4381 GCAGGGGGGCTGCCTCTCCACAAAGAAAAACAAACACTGCAGATATCCTTCAGGACCTG 4440  
 |||||  
 Db 4381 GCAGGGGGGCTGCCTCTCCACAAAGAAAAACAAACACTGCAGATATCCTTCAGGACCTG 4440  
 Qy 4441 ACAGGAAGAAACATTTTCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500

Db	4441		ACAGGAAGAAACATTT	CGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4500
Qy	4501		TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCACT	4560	
Db	4501		TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCACT	4560	
Qy	4561		AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620	
Db	4561		AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620	
Qy	4621		CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4680	
Db	4621		CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4680	
Qy	4681		ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740	
Db	4681		ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740	
Qy	4741		GCAATCAGCTCTTTCTGAATGTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAAG	4800	
Db	4741		GCAATCAGCTCTTTCTGAATGTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAAG	4800	
Qy	4801		GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG	4860	
Db	4801		GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG	4860	
Qy	4861		CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT	4920	
Db	4861		CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT	4920	
Qy	4921		GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTGCTATTCCTGATCCAGGAGCGG	4980	
Db	4921		GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTGCTATTCCTGATCCAGGAGCGG	4980	
Qy	4981		GTCAGCAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040	
Db	4981		GTCAGCAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040	
Qy	5041		TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100	
Db	5041		TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100	
Qy	5101		TTCATCTGCTTCCAGCAGAAGTCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTT	5160	
Db	5101		TTCATCTGCTTCCAGCAGAAGTCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTT	5160	
Qy	5161		CTACTTTTGTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220	
Db	5161		CTACTTTTGTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220	
Qy	5221		AAGATCCCCAGCACAGCCTATGTGGTGCTACCCAGCGTGAACCTCTTCATTGGCATTAAAT	5280	
Db	5221		AAGATCCCCAGCACAGCCTATGTGGTGCTACCCAGCGTGAACCTCTTCATTGGCATTAAAT	5280	
Qy	5281		GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340	
Db	5281		GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340	
Qy	5341		GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTGGCCTGGGACGAGGGCTCATC	5400	
Db	5341		GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTGGCCTGGGACGAGGGCTCATC	5400	
Qy	5401		GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460	
Db	5401		GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460	
Qy	5461		GTGTCAACCATTTCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520	
Db	5461		GTGTCAACCATTTCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520	

Qy 5521 GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT 5580  
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 Db 5521 GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT 5580

Qy 5581 GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG 5640  
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 Db 5581 GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG 5640

Qy 5641 AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700  
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 Db 5641 AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700

Qy 5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTGCGTGGGCATTCTCCTGCTGAG 5760  
 |||  
 Db 5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTGCGTGGGCATTCTCCTGCTGAG 5760

Qy 5761 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAATCATCAACTTTCAAGATGTTAACA 5820  
 |||  
 Db 5761 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAATCATCAACTTTCAAGATGTTAACA 5820

Qy 5821 GGAGATACCACTGTTACCAGAGGAGATGCTTCTTAACAGAAATAGTATCTTATCAAAC 5880  
 |||  
 Db 5821 GGAGATACCACTGTTACCAGAGGAGATGCTTCTTAACAGAAATAGTATCTTATCAAAC 5880

Qy 5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940  
 |||  
 Db 5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940

Qy 5941 TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCAGAGAAAGAA 6000  
 |||  
 Db 5941 TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCAGAGAAAGAA 6000

Qy 6001 GTTGGCAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCTCGTGAAGTATGGAGAAAA 6060  
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 Db 6001 GTTGGCAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCTCGTGAAGTATGGAGAAAA 6060

Qy 6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6120  
 |||  
 Db 6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6120

Qy 6121 GCGGGCCTCCTGTGGTGTCTTGATGAACCCACCACAGGCATGCCAAAGCCCGG 6180  
 |||  
 Db 6121 GCGGGCCTCCTGTGGTGTCTTGATGAACCCACCACAGGCATGCCAAAGCCCGG 6180

Qy 6181 CGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTCTTACA 6240  
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 Db 6181 CGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTCTTACA 6240

Qy 6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6300  
 |||  
 Db 6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6300

Qy 6301 AGGTTCAAGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA 6360  
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 Db 6301 AGGTTCAAGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA 6360

Qy 6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6420  
 |||  
 Db 6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6420

Qy 6421 CTGCAATTCCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT 6480  
 |||  
 Db 6421 CTGCAATTCCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT 6480

Qy 6481 CCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCAGAGCAAAAAGCGA 6540  
 |||  
 Db 6481 CCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCAGAGCAAAAAGCGA 6540

Qy 6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT 6600  
 |||  
 Db 6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT 6600



Qy 6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660  
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 Db 6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660  
 |||  
 Qy 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6720  
 |||  
 Db 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6720  
 |||  
 Qy 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTTCCTTT 6780  
 |||  
 Db 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGNACTAGACTTTTCCTTT 6780  
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 Qy 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840  
 |||  
 Db 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840  
 |||  
 Qy 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880  
 |||  
 Db 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880  
 |||

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	6880	100.0	6880	21	AAZ94734	Human ATP binding
2	6880	100.0	6880	22	AAI70314	Human ATP binding
3	6880	100.0	7260	22	AAD21326	Human ATP binding
4	6880	100.0	7260	22	AAI70315	Human ATP binding
5	6879	100.0	9497	24	ABV78020	Hypoxia-regulated
6	6876.8	100.0	6880	22	AAD21325	Human ATP binding
7	6875.8	99.9	9741	22	AAS06120	Human ABC1 DNA seq
8	6875.8	99.9	9741	24	AAD37273	Human ABC1 full-le
9	6875.8	99.9	9854	22	AAS06121	Human ABC1 DNA seq
10	6875.8	99.9	9870	24	ABN99301	Polymorphic human
11	6875.8	99.9	9870	24	ABN99302	Polymorphic human
12	6875.8	99.9	9870	24	ABN99303	Polymorphic human
13	6875.8	99.9	9870	24	ABN99324	Polymorphic human
14	6875.8	99.9	9870	24	ABN99328	Polymorphic human
15	6875.8	99.9	9870	24	ABN99329	Polymorphic human
16	6875.8	99.9	9870	24	ABN99330	Polymorphic human
17	6875.8	99.9	9870	24	ABN99331	Polymorphic human
18	6875.8	99.9	9870	24	ABN99332	Polymorphic human
19	6875.8	99.9	9870	24	ABN99333	Polymorphic human
20	6875.8	99.9	9870	24	ABN99334	Polymorphic human
21	6875.8	99.9	9870	24	ABN99335	Polymorphic human
22	6875.2	99.9	7281	22	AAK51683	Human polynucleoti
23	6874.2	99.9	9741	24	ABL58146	Human ABCA1 transp
24	6874.2	99.9	9870	24	ABN99304	Polymorphic human
25	6874.2	99.9	9870	24	ABN99305	Polymorphic human
26	6874.2	99.9	9870	24	ABN99306	Polymorphic human
27	6874.2	99.9	9870	24	ABN99307	Polymorphic human
28	6874.2	99.9	9870	24	ABN99309	Polymorphic human
29	6874.2	99.9	9870	24	ABN99310	Polymorphic human
30	6874.2	99.9	9870	24	ABN99311	Polymorphic human
31	6874.2	99.9	9870	24	ABN99312	Polymorphic human
32	6874.2	99.9	9870	24	ABN99313	Polymorphic human
33	6874.2	99.9	9870	24	ABN99314	Polymorphic human
34	6874.2	99.9	9870	24	ABN99315	Polymorphic human
35	6874.2	99.9	9870	24	ABN99316	Polymorphic human
36	6874.2	99.9	9870	24	ABN99317	Polymorphic human
37	6874.2	99.9	9870	24	ABN99318	Polymorphic human
38	6874.2	99.9	9870	24	ABN99319	Polymorphic human
39	6874.2	99.9	9870	24	ABN99320	Polymorphic human
40	6874.2	99.9	9870	24	ABN99321	Polymorphic human
41	6874.2	99.9	9870	24	ABN99322	Polymorphic human
42	6874.2	99.9	9870	24	ABN99323	Polymorphic human
43	6874.2	99.9	9870	24	ABN99325	Polymorphic human
44	6874.2	99.9	9870	24	ABN99326	Polymorphic human

45 6874.2 99.9 9870 24 ABN99327

Polymorphic human

# SUMMARIES

RESULTS							
Result	%		Query				
No.	Score	Match	Length	DB	ID	Description	
-----							
1	430.8	6.3	5894	3	US-08-665-259-24	Sequence 24, Appl	
2	430.8	6.3	5894	3	US-08-762-500-24	Sequence 24, Appl	
3	430.8	6.3	6525	3	US-08-762-500-74	Sequence 74, Appl	
4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap	
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap	
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap	
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap	
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap	
c 9	83.8	1.2	2253	4	US-09-252-991A-3810	Sequence 3810, Ap	
10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App	
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap	
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap	
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap	
15	75	1.1	1770	4	US-09-328-352-3466	Sequence 3466, Ap	

# SUMMARIES

Result		Query						
No.	Score	Match	Length	DB	ID	Description		
	1	3600.4	52.3	4783	11	AK051920	AK051920 Mus muscu	
	2	1024.8	14.9	3605	11	AK052916	AK052916 Mus muscu	
	3	692.4	10.1	809	12	BI754756	BI754756 603025477	
	4	636.6	9.3	854	12	BI854140	BI854140 603381449	
	5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GIO-	
c	6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-	
	7	587.8	8.5	673	14	CD351490	CD351490 UI-M-GIO-	
c	8	550.4	8.0	661	14	CB481810	CB481810 jns83_A02	
	9	547.6	8.0	773	14	CB526974	CB526974 UI-M-FY0-	
	10	542	7.9	837	10	BF160011	BF160011 601768192	
	11	536.8	7.8	652	10	BB468374	BB468374 BB468374	
	12	535.2	7.8	702	12	BI658600	BI658600 603284335	
	13	532.4	7.7	724	12	BG920223	BG920223 602822304	
c	14	528.4	7.7	639	14	CB477340	CB477340 jns20_C11	
	15	525	7.6	720	12	BI248317	BI248317 602966918	
	16	516	7.5	620	14	CA889361	CA889361 B0152D10-	
	17	510.4	7.4	512	13	BX279856	BX279856 BX279856	
c	18	505	7.3	614	14	CB478239	CB478239 jns32_B02	
	19	486.4	7.1	605	14	CB546553	CB546553 AMGNNUC:N	
	20	479.8	7.0	579	14	CA884367	CA884367 B0109G01-	
	21	477	6.9	1004	11	BC034824	BC034824 Homo sapi	
	22	473	6.9	562	10	BE665489	BE665489 154542 MA	
	23	459.4	6.7	515	10	BF094524	BF094524 MR0-UT004	
	24	456.8	6.6	605	14	CB581583	CB581583 AMGNNUC:N	
	25	447.6	6.5	554	10	BF076322	BF076322 225856 MA	
	26	438.4	6.4	512	14	CB717058	CB717058 AMGNNUC:N	
	27	435.6	6.3	884	13	BU906084	BU906084 AGENCOURT	

## RESULT 1

AK051920

LOCUS AK051920 4783 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230019D04 product:ATP-binding cassette, sub-family A (ABC1), member 1, full insert sequence.

ACCESSION AK051920

VERSION AK051920.1 GI:26342297

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,  
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,  
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.  
and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4783)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source

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ORIGIN

Query Match 52.3%; Score 3600.4; DB 11; Length 4783;  
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 Db 301 IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 360  
 Qy 1187 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDIPESRETD 1246  
 Db 361 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDIPESRETD 420  
 Qy 1247 LLSGMDGKGSYQVKGWKLTTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 1306  
 Db 421 LLSGMDGKGSYQVKGWKLTTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 480  
 Qy 1307 IVPPFGKYPSLELQPMWYNEQYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPIPD 1366  
 Db 481 IVPPFGKYPSLELQPMWYNEQYTFVSNDAPEDMGTQELNALT KDPGFGTRCMEGNPIPD 540  
 Qy 1367 TPCQAGEEWTAPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426  
 Db 541 TPCQAGEEWTAPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600  
 Qy 1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 1486  
 Db 601 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 660  
 Qy 1487 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546  
 Db 661 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 720  
 Qy 1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 1606  
 Db 721 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 780  
 Qy 1607 FVPASFVVFLIQERVSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQQ 1666  
 Db 781 FVPASFVVFLIQERVSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQQ 840  
 Qy 1667 KSYVSSTNLPLVALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726  
 Db 841 KSYVSSTNLPLVALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900  
 Qy 1727 VLELFTDNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786  
 Db 901 VLELFTDNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960  
 Qy 1787 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846  
 Db 961 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1020  
 Qy 1847 GQNDILEIKELTKIYRRKRKPAVDRI CVGIPPGECFGLLG VNGAGKSTTFKMLTGDITVT 1906  
 Db 1021 GQNDILEIKELTKIYRRKRKPAVDRI CVGIPPGECFGLLG VNGAGKSTTFKMLTGDITVT 1080  
 Qy 1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVG 1966  
 Db 1081 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVG 1140  
 Qy 1967 WAIRKGLVKYGEKYAGNYSGGNKRKLSTAMALIGPPVVFLEPTTGMDPKARRFLWNC 2026

Db	1141	WAIRKLGVLVYKEGYASNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC	1200
Qy	2027	ALSVVKEGRSVVLTSHEMEECEALCTRMAMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA	2086
Db	1201	ALSIVKEGRSVVLTSHEMEECEALCTRMAMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA	1260
Qy	2087	GSNPDLKPVDFFGLAFPGSVPEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDY	2146
Db	1261	GSNPDLKPVEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDY	1320
Qy	2147	SVSQTTLDQVFNFAKDQSDDDLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2201
Db	1321	SVSQTTLDQVFNFAKDQSDDDLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	1375

Query Match 60.2%; Score 6909; DB 3; Length 1375:

Best Local Similarity 96.9%; Pred. No. 0;  
Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

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Qy      827 CMEEEPHTHLKLGVSIGNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886
      |||:|||||
Db      1 CMEEEPHTHLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy      887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKGLSEK 946
      |||:|||||
Db      61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKGLSEK 120

Qy      947 HVKAEMEQMALDVGLPPSKLKSQTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 1006
      |||:|||||
Db      121 HVKAEMEQMALDVGLPPSKLKSQTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180

Qy     1007 SRRGIWELLKLYRQGRTIILSTHMHDEADVLDRIAIIISHGKLCCVGSSSLFLKNQLGTGY 1066
      |||:|||||
Db      181 SRRGIWELLKLYRQGRTIILSTHMHDEADILGRIAIIISHGKLCCVGSSSLFLKNQLGTGY 240

Qy     1067 YLTLVKKDVESLSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDESHTLTIDVSAISNL 1126
      |||:|||||
Db      241 YLTLVKKDVESLSLSSCRNSSSTVSCLKKEDSVSQSSSDAGLGSDESHTLTIDVSAISNL 300

Qy     1127 IRKHVSEARLVEDIGHELTIVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 1186
      |||:|||||
Db      301 IRKHVSEARLVEDIGHELTIVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 360

Qy     1187 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETD 1246
      |||:|||||
Db      361 IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLHPFTEDDAVDPNDSIDPESRETD 420

Qy     1247 LLSGMDGKGSYQVKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 1306
      |||:|||||
Db      421 LLSGMDGKGSYQLKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 480

Qy     1307 IVPFGKYPSELEQPMWYNEQYTFVSNDAPEDTGTLELLNALT KDPGFGRCEMGNPIPD 1366
      |||:|||||
Db      481 IVPFGKYPSELEQPMWYNEQYTFVSNDAPEDMGTQELNALT KDPGFGRCEMGNPIPD 540

Qy     1367 TPCQAGEEWTTPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
      |||:|||||
Db      541 TPCQAGEEDWTISVPVQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600

Qy     1427 PQRKQNTADILQDLTGRNISDYLKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNTQALP 1486
      |||:|||||
Db      601 PQRKQKTADILQNL TGRNISDYLKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNSQALP 660

Qy     1487 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
      |||:|||||
Db      661 PSHEVNDAIKQMKKLLKTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL 720

Qy     1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMS 1606
      |||:|||||
Db      721 NVINNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMS 780

Qy     1607 FVPASFVVFLIQERVSKAKHLQFISGVKPVIIYWSNFVWDMCNYVVPATLVIIIFICFQQ 1666
      |||:|||||
Db      781 FVPASFVVFLIQERVSKAKHLQFISGVKPVIIYWSNFVWDMCNYVVPATLVIIIFICFQQ 840

Qy     1667 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
      |||:|||||
Db      841 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900

Qy     1727 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786
      |||:|||||
Db      901 VLELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960

Qy     1787 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
      |||:|||||
Db      961 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGG 1020
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Qy 1847 GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGEFCGLLVNGAGKSSTFKMLTGDTT VT 1906  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1021 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGEFCGLLVNGAGKSSTFKMLTGDT PVT 1080  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE 1966  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1081 RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGK FGE 1140  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 1967 WAIRKGLVLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC 2026  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1141 WAIRKGLVLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC 1200  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 2027 ALSVVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1201 ALSIVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 2087 GSNPDLKPVQDFFGLAFFPGSVPEKEHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 2146  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1261 GSNPDLKPVQEFFGLAFFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 1320  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 2147 SVSQTTLDQVFVNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1321 SVSQTTLDQVFVNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

# SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	10906	95.1	2201	2	A54774		ATP binding cassette
2	3338.5	29.1	1529	2	A59189		ATP-binding cassette
3	3129.5	27.3	1472	2	B54774		ATP binding cassette
4	2638.5	23.0	1704	2	S71363		probable ATP-binding
5	2635.5	23.0	1704	2	A59188		ATP-binding cassette
6	2061	18.0	1802	2	T33783		hypothetical prote
7	1975	17.2	1816	2	A84845		probable ABC trans
8	1854.5	16.2	1447	2	T15200		hypothetical prote
9	1792	15.6	1317	2	C88925		protein F33E11.4 [
10	1535.5	13.4	1758	2	F88559		protein C48B4.4b [
11	1528.5	13.3	1704	2	T42749		ATP-binding cassette
12	1526	13.3	1767	2	S60124		transport protein
13	1393	12.1	1246	2	T00826		hypothetical prote
14	1150.5	10.0	1564	2	T27121		hypothetical prote
15	1006.5	8.8	373	2	T47150		hypothetical prote
16	1005.5	8.8	1431	2	T22748		hypothetical prote
17	846	7.4	269	2	T46467		hypothetical prote
18	786.5	6.9	1011	2	T07712		probable ABC-type
19	695	6.1	900	2	T07717		probable ABC-type

## RESULT 1

A54774

ATP binding cassette transporter ABC1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Apr-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Feb-2001

C;Accession: A54774

R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.

Genomics 21, 150-159, 1994

A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.

A;Reference number: A54774; MUID:94375008; PMID:8088782

A;Accession: A54774

A;Molecule type: mRNA

A;Residues: 1-2201 <LUC>

A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C;Keywords: ATP; duplication; nucleotide binding; P-loop

F;856-1047/Domain: ATP-binding cassette homology <ABC1>

F;873-880/Region: nucleotide-binding motif A (P-loop)

F;1869-2060/Domain: ATP-binding cassette homology <ABC2>  
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 95.1%; Score 10906; DB 2; Length 2201;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

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Qy      1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLYSQKDT 60
        |||
Db      1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLYSQRDT 60

Qy     61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
        |||
Db     61 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLQXNVGLQ 120

Qy    121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAAAERVLSNMDILKPIL 180
        |||
Db    121 KVFLQGYQLHLASLCNGSKLEBIIQLGDAEVSALCGLPRKKLDAAEVRLRYNMDILKPVV 180

Qy    181 RTLNSTSPFPSEKELAEATKTLHSLGTLAQELFSMRSWSDMRQEVMTNVSSTSTQI 240
        |||
Db    181 TKLNSTSHLPTQHLAEATTVLDSLGLAQELFSTKSWSDMRQEVMTNVSSTSTQI 240

Qy    241 YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFDNSTTPYCNDLMK 300
        |||
Db    241 YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNTEEDVDTFDNSTTPYCNDLMK 300

Qy    301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 360
        |||
Db    301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 360

Qy    361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTADQDIVAFLAKHPEDVQSSNGS 420
        |||
Db    361 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTADQDIMAFLAKNPEDVQSPNGS 420

Qy    421 VYTWREAFNETNQAIQTISRMECVNLNKLPIATEVWLINKSMELLDERKFWAGIVFTG 480
        |||
Db    421 VYTWREAFNETNQAIQTISRMECVNLNKLPIATEVWLINKSMELLDERKFWAGIVFTG 480

Qy    481 ITPGSIELPHHVYKIRMDIDNVERTNKKIDGYWDGPRADPFEDMRYVWGGFAYLQDVV 540
        |||
Db    481 ITPDSVELPHHVYKIRMDIDNVERTNKKIDGYWDGPRADPFEDMRYVWGGFAYLQDVV 540

Qy    541 EQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKIV 600
        |||
Db    541 EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIISIV 600

Qy    601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAAGLLVILKGNLLPYSDPSVVFV 660
        |||
Db    601 YEKEARLKETMRIMGLDNGILWFSWVSSLIPLLVSAAGLLVILKGNLLPYSDPSVVFV 660

Qy    661 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
        |||
Db    661 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 720

Qy    721 LLSPVAFGFGCEYFALFEEQGIGVQWQDNLFESPVVEEDGFNLTSVSMMLFDFTLYGVMTW 780
        |||
Db    721 LLSPVAFGFGCEYFALFEEQGIGVQWQDNLFESPVVEEDGFNLTAVSMMMLFDFTLYGVMTW 780

Qy    781 YIEAVFPGQYGIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISICMEEEPHTLKLGV 840
        |||
Db    781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHTLKLGV 840

Qy    841 IQNLVKVYRDGMKVAVDGLALNFYEQITSFLGHNGAGKTTMSILTGLFPPTSGTAYIL 900
        |||
Db    841 IQNLVKVYRDGMKVAVDGLALNFYEQITSFLGHNGAGKTTMSILTGLFPPTSGTAYIL 900

Qy    901 GKDIRSEMSTIRQNLGVCPQHNVLPDMLTVEEHIWFYARLKGLSEKHVKAEMEQLMADV 960
        |||
Db    901 GKDIRSEMSSIRQNLGVCPQHNVLPDMLTVEEHIWFYARLKGLSEKHVKAEMEQLMADV 960
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QY	961	LPSSKLSKTSQLSGGMQRKLSVALAFVGGSKVVLDEPTAGVDPYSRRGIWELLKKYRQ	1020
Db	961	LPPSKLSKTSQLSGGMQRKLSVALAFVGGSKVVLDEPTAGVDPYSRRGIWELLKKYRQ	1020
QY	1021	GRTIILSTHHMDEADVLDGRIAIISHGKLCVVGSSFLFNQLGTGYLTLVKKDVESLS	1080
Db	1021	GRTIILSTHHMDEADVLDGRIAIISHGKLCVVGSSFLFNQLGTGYLTLVKKDVESLS	1080
QY	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKHVSEARLVEDI	1140
Db	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKHVSEARLVEDI	1140
QY	1141	GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE	1200
Db	1141	GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE	1200
QY	1201	TSDGTLFARRNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETDLGSGMDGKGSYQVK	1260
Db	1201	TSDGTLFARRNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETDLGSGMDGKGSYQVK	1260
QY	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
Db	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
QY	1321	PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEWTTP	1380
Db	1321	PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEWTTP	1380
QY	1381	VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL	1440
Db	1381	VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL	1440
QY	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK	1500
Db	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK	1500
QY	1501	HLKLAKDSSADRFNLNLSGRFMGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
Db	1501	HLKLAKDSSADRFNLNLSGRFMGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
QY	1561	GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSIICVIFAMSFVPASFVFLIQR	1620
Db	1561	GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSIICVIFAMSFVPASFVFLIQR	1620
QY	1621	VSKAKHLQFISGVKPIYWLSNFWDMCNVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
Db	1621	VSKAKHLQFISGVKPIYWLSNFWDMCNVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
QY	1681	LLLLYGSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN	1740
Db	1681	LLLLYGSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN	1740
QY	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG	1800
Db	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG	1800
QY	1801	VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Db	1801	VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
QY	1861	YRRKRKPAVDRIICVIGIPPGECFGLLVGNAGKSTTFKMLTGDTTVTRGDAFLNKNLSILN	1920
Db	1861	YRRKRKPAVDRIICVIGIPPGECFGLLVGNAGKSTTFKMLTGDTTVTRGDAFLNKNLSILN	1920
QY	1921	IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKGEWAIRKLGVLKYGEK	1980
Db	1921	IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKGEWAIRKLGVLKYGEK	1980
QY	1981	YAGNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	1981	YAGNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040



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Qy      2041 SHSMEECEALCTRMAMVNGRFRCLGSGVQHLKNRFGDGYTIVVRIAGSNPDLKPVDFFG 2100
        |||
Db      2041 SHSMEECEALCTRMAMVNGRFRCLGSGVQHLKNRFGDGYTIVVRIAGSNPDLKPVEFFG 2100

Qy      2101 LAFPGSVKPEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLQVFN 2160
        |||
Db      2101 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLQVFN 2160

Qy      2161 AKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
        |||
Db      2161 AKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201

```

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477 homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758 homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.3	343	1	NODI_RHISN	P55476 rhizobium s
10	366	3.2	304	1	NODI_RHIS3	P72335 rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879 escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	344.5	3.0	340	1	NODI_RHILO	P23703 rhizobium l
14	343.5	3.0	347	1	NODI_RHIGA	P50332 rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183 homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618 rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776 escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624 escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447 mus musculu

## RESULT 2

### ABC1\_MOUSE

ID ABC1\_MOUSE STANDARD; PRT; 2261 AA.

AC P41233;

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette

DE transporter 1) (ATP-binding cassette 1) (ABC-1).

GN ABCA1 OR ABC1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2; TISSUE=Macrophage;

RX MEDLINE=94375008; PubMed=8088782;

RA Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;

RT "Cloning of two novel ABC transporters mapping on human chromosome

RT 9.";

RL Genomics 21:150-159(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RX MEDLINE=21251004; PubMed=11352567;

RA Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;

RT "Human and mouse ABCA1 comparative sequencing and transgenesis

RT studies revealing novel regulatory sequences.";

RL Genomics 73:66-76(2001).

CC -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION

CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL

CC TRANSPORT (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST

CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.

CC -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,

CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN

CC ATP BINDING CASSETTE (ABC) DOMAIN.

CC -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By

CC similarity).

CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.

CC -----

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DR EMBL; X75926; CAA53530.1; ALT\_INIT.

DR EMBL; AF287263; AAG39073.1; ALT\_INIT.

DR MGD; MGI:99607; Abcal.

DR GO; GO:0008203; P:cholesterol metabolism; IDA.

DR GO; GO:0030301; P:cholesterol transport; IDA.

DR InterPro; IPR003593; AAA\_ATPase.

DR InterPro; IPR003439; ABC\_transporter.

DR Pfam; PF00005; ABC\_tran; 2.

DR ProDom; PD000006; ABC\_transporter; 2.

DR SMART; SM00382; AAA; 2.

DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.

DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 2.

KW ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.

FT	TRANSMEM	26	42	POTENTIAL.
FT	TRANSMEM	640	656	POTENTIAL.
FT	TRANSMEM	690	706	POTENTIAL.
FT	TRANSMEM	717	733	POTENTIAL.
FT	TRANSMEM	749	765	POTENTIAL.
FT	TRANSMEM	771	787	POTENTIAL.
FT	TRANSMEM	1041	1057	POTENTIAL.
FT	TRANSMEM	1351	1367	POTENTIAL.
FT	TRANSMEM	1661	1677	POTENTIAL.
FT	TRANSMEM	1708	1724	POTENTIAL.
FT	TRANSMEM	1737	1753	POTENTIAL.
FT	TRANSMEM	1775	1791	POTENTIAL.
FT	TRANSMEM	1854	1870	POTENTIAL.
FT	NP_BIND	933	940	ATP (POTENTIAL).
FT	NP_BIND	1946	1953	ATP (POTENTIAL).
FT	MOD_RES	1042	1042	PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT				SIMILARITY).
FT	MOD_RES	2054	2054	PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT				SIMILARITY).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	820	820	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1144	1144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1294	1294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1453	1453	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	1499	1499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1504	1504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1637	1637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2238	2238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1567	1568	MISSING (IN REF. 2).
FT	CONFLICT	2024	2024	MISSING (IN REF. 2).
SQ	SEQUENCE	2261	AA; 254011 MW; FAE62B21FD1D09F9 CRC64;	

Query Match 95.1%; Score 10906; DB 1; Length 2261;  
 Best Local Similarity 94.8%; Pred. No. 0;  
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFS	DARRLLYSQKDT	60
Db	61	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLLSQKDT	120	
Qy	61	SMKDMRKVLRLTLQQIKSSSNLKLQDFLVDNETFSGFLYHNLSL	PKSTVDKMLRADVILH	120
Db	121	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNSL	PRSTVDSLLQXNVGLQ	180
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELGCLPREKLA	AERVLRSNMDILKPIL	180
Db	181	KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKL	DAAERVLRYNMDILKPVV	240
Qy	181	RTLNSTSPFPKSELAEATKTLHLGLTQELFSMRSWSDMRQEV	MFLTNVSSSSSTQI	240
Db	241	TKLNSTSHLPTQHLAEATTVLLDSLGLAQELFSTKSWSDMRQEV	MFLTNVSSSSSTQI	300
Qy	241	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDA	ETFYDNSTTPYCNDLMK	300
Db	301	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNTEEDVD	TFYDNSTTPYCNDLMK	360
Qy	301	NLESSPLSRIIWKALKPPLLVGKILYTPDTPATRVMAEVNKT	FQELAVFHDLEGMWEELS	360
Db	361	NLESSPLSRIIWKALKPPLLVGKILYTPDTPATRVMAEVNKT	FQELAVFHDLEGMWEELS	420
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWT	AQDIVAFLAKHPEDVQSSNGS	420
Db	421	PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWT	AQDIMAFIAKHPEDVQSPNGS	480
Qy	421	VYTWREAFNETNQAIQTISRMECVNLNLEPIATEVWL	LINKSMELDERKFWAGIVFTG	480
Db	481	VYTWREAFNETNQAIQTISRMECVNLNLEPIATEVWL	LINKSMELDERKFWAGIVFTG	540
Qy	481	ITPGSIELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRAD	PFEDMRVWGGFAYLQD	540
Db	541	ITPDSVELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRAD	PFEDMRVWGGFAYLQD	600
Qy	541	EQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSR	SMPLEFMTLAWIYSVAVI	600
Db	601	EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSR	SMPLEFMTLAWIYSVAVI	660
Qy	601	YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLV	SAGLLVVLKGNLLPYSDPSVVFV	660
Db	661	YEKEARLKETMRIMGLDNGILWFSWFISSLIPLLV	SAGLLVVLKGNLLPYSDPSVVFV	720
Qy	661	FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFT	LYLPYVLCVAWQDYVGFTL	720
Db	721	FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFT	LYLPYVLCVAWQDYVGFSIKIFAS	780
Qy	721	LLSPVAFGFGCEYFALFEEQIGVQWDLNLFESPVEED	GFNLTTSVSMMLFDTFLYG	780
Db	781	LLSPVAFGFGCEYFALFEEQIGVQWDLNLFESPVEED	GFNLTTAVSMMLFDTFLYG	840
Qy	781	YIEAVFPGQYGIPRPWFYFCTKSYWFGEESEKSH	PGSNQKRISICMEEEP	840
Db	841	YIEAVFPGQYGIPRPWFYFCTKSYWFGEESEKSH	PGSSQKGVSEICMEEEP	900
Qy	841	IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAG	KTMTTMSILTGLFPPTSGTAYIL	900

Db 901 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960  
 Qy 901 GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKLGLSEKHVKAEMEQMALDVG 960  
 Db 961 GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKLGLSEKHVKAEMEQMALDVG 1020  
 Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKLYRQ 1020  
 Db 1021 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKLYRQ 1080  
 Qy 1021 GRTIILSTHHMDEADVLDRIAIIISHGKLCCVGSSLFLKNQLGTGYLTLVKKDVESSLS 1080  
 Db 1081 GRTIILSTHHMDEADILGDRIAIIISHGKLCCVGSSLFLKNQLGTGYLTLVKKDVESSLS 1140  
 Qy 1081 SCRNSSTVSYLKKEDEVSSQSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDI 1140  
 Db 1141 SCRNSSTVSCLKKEDEVSSQSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDI 1200  
 Qy 1141 GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200  
 Db 1201 GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1260  
 Qy 1201 TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLLSGMDGKGSYQVK 1260  
 Db 1261 TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLLSGMDGKGSYQVK 1320  
 Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ 1320  
 Db 1321 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ 1380  
 Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEETWTP 1380  
 Db 1381 PWMYNEQYTFVSNDAPEDMGTQELLNALTDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440  
 Qy 1381 VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440  
 Db 1441 VPQSVIDLQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQNL 1500  
 Qy 1441 TGRNISDYLVKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500  
 Db 1501 TGRNISDYLVKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560  
 Qy 1501 HLKLAKDSSADRFNLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNINNAILRANLQK 1560  
 Db 1561 LLKLTKDTSADRFNLNSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNINNAILRANLQK 1620  
 Qy 1561 GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1620  
 Db 1621 GENPSQYGITAFNHPLNLTQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1680  
 Qy 1621 VSKAKHLQFISGVKPVIIYWLSNFWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVLAL 1680  
 Db 1681 VSKAKHLQFISGVKPVIIYWLSNFWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVLAL 1740  
 Qy 1681 LLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN 1740  
 Db 1741 LLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNIN 1800  
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG 1800  
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG 1860  
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860  
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920  
 Qy 1861 YRRKRKPAVDRICIGIPPGEFCGLLVGAGKSTTFKMLTGDTPVTRGDAFLNRNSILSN 1920  
 Db 1921 YRRKRKPAVDRICIGIPPGEFCGLLVGAGKSTTFKMLTGDTPVTRGDAFLNRNSILSN 1980  
 Qy 1921 IHEVHQNMGYCPQFDAQTELLTGREHVEFFALLRGVPEKEVGKVGWAIKRLGLVKYGEK 1980

Db	1981	IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGLVKYGEK	2040
Qy	1981	YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	2041	YASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT	2100
Qy	2041	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG	2100
Db	2101	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG	2160
Qy	2101	LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF	2160
Db	2161	LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF	2220
Qy	2161	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2201
Db	2221	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2261